

SCORE Search Results Details for Application 10617561 and Search Result us-10-617-561-15.p2n.rng.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:32:04 ; Search time 332.409 Seconds
(without alignments)
1038.259 Million cell updates/sec

Title: US-10-617-561-15
Perfect score: 169
Sequence: 1 XHWSHDWKPGFALALKALKKKALKKKLKKALKKKAL 33

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

```
-MODEL=frame+_p2n.model -DEV=xlp  
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102051_79/app_query.fasta_1  
-DB=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p  
-USER=US10617561@CGN_1_1_1975@runat_11082006_102051_79 -NCPU=6 -ICPU=3  
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120  
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : N_Geneseq_8:*
1: geneseqn1980s:*

2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002as:*
 7: geneseqn2002bs:*
 8: geneseqn2003as:*
 9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004as:*
 13: geneseqn2004bs:*
 14: geneseqn2005s:*
 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Match	Query Length	DB	ID	Description
	1	80	47.3	750	12	ADG83792	Adg83792 Lamprey p
	2	76	45.0	718	12	ADG83794	Adg83794 Lamprey p
	3	75	44.4	790	12	ADG83788	Adg83788 Lamprey p
	4	69	40.8	676	12	ADG83790	Adg83790 Lamprey p
c	5	66	39.1	161334	11	ACN44334	Acn44334 Human gen
c	6	64.5	38.2	1730	2	AAQ44429	Aaq44429 Kcal-1.8
c	7	64.5	38.2	1730	2	AAT61043	Aat61043 Porcine a
c	8	63.5	37.6	413	8	ABX36485	Abx36485 Bovine ES
	9	63.5	37.6	431	8	ABX39359	Abx39359 Bovine ES
	10	61	36.1	648	10	ABZ40693	Abz40693 N. gonorr
	11	61	36.1	132942	14	ADZ12611	Adz12611 Murine ca
c	12	60.5	35.8	1542	6	ABK35258	Abk35258 Human cDN
c	13	60.5	35.8	1549	10	ADI15977	Adi15977 Human PP
c	14	60.5	35.8	1549	12	ADJ81703	Adj81703 Tumour an
c	15	60.5	35.8	1668	14	AED18045	Aed18045 Fibrotic
c	16	60.5	35.8	1765	10	ADJ56437	Adj56437 Human cDN
c	17	60.5	35.8	2045	12	ADJ62780	Adj62780 Human cDN
c	18	60.5	35.8	2045	14	ADX07279	Adx07279 Cyclin-de
c	19	60.5	35.8	2138	11	ACN88839	Acn88839 Breast ca
	20	60	35.5	111	10	ABZ40692	Abz40692 N. gonorr
	21	60	35.5	742	5	AAS72405	Aas72405 DNA encod
	22	60	35.5	1644	6	ABK49105	Abk49105 Human cDN
	23	60	35.5	13608	4	AAK87529	Aak87529 Human imm
	24	60	35.5	20001	13	ADT77140	Adt77140 Type II d
c	25	60	35.5	21761	4	ABK42793	Abk42793 Genomic s
c	26	60	35.5	21761	4	AAK66660	Aak66660 Human imm
c	27	60	35.5	21761	9	ADB60949	Adb60949 Connectiv
	28	60	35.5	48275	3	AAA81501	Aaa81501 N. mening
c	29	60	35.5	110000	3	AAA81489_0	Aaa81489 N. mening
c	30	60	35.5	349980	3	AAF21610	Aaf21610 Neisseria
	31	59.5	35.2	363	6	AAD25405	Aad25405 Human gon
	32	59.5	35.2	363	8	AAD53500	Aad53500 Human gon
	33	59.5	35.2	363	14	ADV43766	Adv43766 Human psy
	34	59.5	35.2	423	9	AAL62565	Aal62565 Human gon
	35	59.5	35.2	1142	12	ADJ40083	Adj40083 Plant cDN
c	36	59	34.9	186	13	ACF90925	Acf90925 Human SIR
	37	59	34.9	488	10	ADB50985	Adb50985 Primary r

SCORE Search Results Details for Application 10617561 and Search Result us-10-617-561-15.p2n.rni.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:51:34 ; Search time 104.299 Seconds
(without alignments)
888.020 Million cell updates/sec

Title: US-10-617-561-15
Perfect score: 169
Sequence: 1 XHWSHDWKPGFALALKALKKKALKKKLKKALKKKAL 33

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102057_179/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss06p -USER=US10617561_@CGN_1_1_529_@runat_11082006_102057_179 -NCPU=6
-ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				ID	Description
	No.	Score	Match	Length	DB	Query		
	1	80	47.3	750	3	US-10-170-096A-5		Sequence 5, Appli
	2	76	45.0	718	3	US-10-170-096A-7		Sequence 7, Appli
	3	75	44.4	790	3	US-10-170-096A-1		Sequence 1, Appli
	4	69	40.8	676	3	US-10-170-096A-3		Sequence 3, Appli
c	5	64.5	38.2	1730	2	US-07-923-095-1		Sequence 1, Appli
c	6	64.5	38.2	1730	2	US-08-229-511-1		Sequence 1, Appli
c	7	64.5	38.2	1730	2	US-08-314-979-1		Sequence 1, Appli
c	8	64.5	38.2	1730	2	US-08-436-716-1		Sequence 1, Appli
c	9	60.5	35.8	1371	3	US-09-949-016-4550		Sequence 4550, Ap
	10	58	34.3	1221	3	US-09-248-796A-4117		Sequence 4117, Ap
	11	58	34.3	1635	3	US-09-722-377-12		Sequence 12, Appl
c	12	58	34.3	2244	3	US-09-489-039A-911		Sequence 911, App
	13	58	34.3	88036	3	US-09-949-016-15335		Sequence 15335, A
	14	57	33.7	300	2	US-08-668-255-6		Sequence 6, Appli
	15	57	33.7	300	2	US-08-668-255-8		Sequence 8, Appli
	16	57	33.7	360	2	US-08-668-255-4		Sequence 4, Appli
	17	57	33.7	553	3	US-09-148-545-133		Sequence 133, App
	18	57	33.7	553	3	US-09-621-011-133		Sequence 133, App
	19	57	33.7	2029	3	US-10-104-047-874		Sequence 874, App
	20	56.5	33.4	1487	3	US-09-722-971-3		Sequence 3, Appli
	21	56.5	33.4	18705	5	US-09-984-429-463		Sequence 463, App
	22	56.5	33.4	18715	5	US-09-984-429-387		Sequence 387, App
c	23	56.5	33.4	142504	3	US-09-949-016-13693		Sequence 13693, A
c	24	56.5	33.4	142506	3	US-09-949-016-12474		Sequence 12474, A
c	25	56	33.1	16720	3	US-09-902-540-1168		Sequence 1168, Ap
c	26	55	32.5	601	3	US-09-949-016-30307		Sequence 30307, A
c	27	55	32.5	601	3	US-09-949-016-196295		Sequence 196295,
	28	55	32.5	963	3	US-09-902-540-3521		Sequence 3521, Ap
	29	55	32.5	8590	3	US-09-949-016-5562		Sequence 5562, Ap
	30	55	32.5	10300	3	US-09-949-016-636		Sequence 636, App
	31	55	32.5	38575	3	US-09-949-016-17304		Sequence 17304, A
c	32	55	32.5	59319	3	US-09-949-016-16115		Sequence 16115, A
	33	55	32.5	119153	3	US-09-949-016-12378		Sequence 12378, A
	34	54.5	32.2	630	2	US-08-185-414E-1		Sequence 1, Appli
	35	54.5	32.2	2890	3	US-08-848-810-1		Sequence 1, Appli
	36	54.5	32.2	2940	2	US-08-428-415-3		Sequence 3, Appli
	37	54.5	32.2	2940	2	US-08-379-685-3		Sequence 3, Appli
	38	54.5	32.2	2940	2	US-08-854-029-3		Sequence 3, Appli
	39	54.5	32.2	2940	3	US-08-428-762-3		Sequence 3, Appli
	40	54.5	32.2	3118	4	US-09-880-107-3035		Sequence 3035, Ap
c	41	54.5	32.2	36820	3	US-09-949-016-16665		Sequence 16665, A
	42	54.5	32.2	283538	3	US-09-949-016-13506		Sequence 13506, A

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:58:24 ; Search time 1105.86 Seconds
(without alignments)
550.013 Million cell updates/sec

Title: US-10-617-561-15
Perfect score: 169
Sequence: 1 XHWSHDWKPGFALALKALKKKALKKKLKKALKKKAL 33

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102100_235/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss06p
-USER=US10617561_CGN_1_1_5513_runat_11082006_102100_235 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_Main:*

```

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	80	47.3	750	7	US-10-170-096A-5	Sequence 5, Appli
2	80	47.3	750	16	US-11-172-274-5	Sequence 5, Appli
3	76	45.0	718	7	US-10-170-096A-7	Sequence 7, Appli
4	76	45.0	718	16	US-11-172-274-7	Sequence 7, Appli
5	75	44.4	790	7	US-10-170-096A-1	Sequence 1, Appli
6	75	44.4	790	16	US-11-172-274-1	Sequence 1, Appli
7	69	40.8	676	7	US-10-170-096A-3	Sequence 3, Appli
8	69	40.8	676	16	US-11-172-274-3	Sequence 3, Appli
c 9	66	39.1	161334	6	US-10-087-192-730	Sequence 730, App
c 10	63.5	37.6	413	3	US-09-960-352-1650	Sequence 1650, Ap
11	63.5	37.6	431	3	US-09-960-352-4524	Sequence 4524, Ap
c 12	63	37.3	586	9	US-10-425-115-95993	Sequence 95993, A
c 13	62	36.7	464	8	US-10-437-963-69292	Sequence 69292, A
14	62	36.7	1491	8	US-10-335-977-4737	Sequence 4737, Ap
15	62	36.7	1710	8	US-10-335-977-4738	Sequence 4738, Ap
16	61	36.1	232	9	US-10-425-115-90482	Sequence 90482, A
17	61	36.1	648	10	US-10-467-657-5975	Sequence 5975, Ap
c 18	61	36.1	651	9	US-10-425-115-110906	Sequence 110906,
c 19	60.5	35.8	658	10	US-10-956-157-3940	Sequence 3940, Ap
20	60.5	35.8	658	10	US-10-956-157-9175	Sequence 9175, Ap
c 21	60.5	35.8	1400	10	US-10-956-157-6626	Sequence 6626, Ap
c 22	60.5	35.8	1542	3	US-09-822-849A-396	Sequence 396, App
c 23	60.5	35.8	1549	9	US-10-734-049A-321	Sequence 321, App
c 24	60.5	35.8	1765	6	US-10-084-817-243	Sequence 243, App
c 25	60.5	35.8	2045	8	US-10-439-703-50	Sequence 50, Appl
c 26	60.5	35.8	2045	10	US-10-956-157-1391	Sequence 1391, Ap
c 27	60.5	35.8	2138	6	US-10-198-846-9989	Sequence 9989, Ap
28	60.5	35.8	160103	7	US-10-085-117-262	Sequence 262, App
29	60	35.5	111	10	US-10-467-657-5973	Sequence 5973, Ap
c 30	60	35.5	578	9	US-10-425-115-136371	Sequence 136371,
31	60	35.5	742	10	US-10-450-763-8209	Sequence 8209, Ap
c 32	60	35.5	21761	3	US-09-764-847-1680	Sequence 1680, Ap
c 33	60	35.5	21761	6	US-10-092-154-1680	Sequence 1680, Ap
c 34	60	35.5	45045	9	US-10-741-600-17689	Sequence 17689, A
35	60	35.5	48275	10	US-10-915-740A-48	Sequence 48, Appl

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:59:05 ; Search time 134.891 Seconds
(without alignments)
582.767 Million cell updates/sec

Title: US-10-617-561-15
Perfect score: 169
Sequence: 1 XHWSHDWKPGFALALKALKKKALKKKLKKALKKAL 33

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2200221 seqs, 794037843 residues

Total number of hits satisfying chosen parameters: 4400442

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102102_304/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss03p
-USER=US10617561_@CGN_1_1_661_@runat_11082006_102102_304 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_New:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	64	37.9	2468	8	US-11-266-748A-27808	Sequence 27808, A	
2	61	36.1	442	9	US-11-348-413-2009	Sequence 2009, Ap	
3	60.5	35.8	931	8	US-11-266-748A-113960	Sequence 113960,	
c 4	60.5	35.8	931	8	US-11-266-748A-161648	Sequence 161648,	
c 5	60.5	35.8	970	8	US-11-266-748A-191356	Sequence 191356,	
c 6	60.5	35.8	970	8	US-11-266-748A-225772	Sequence 225772,	
c 7	60.5	35.8	993	8	US-11-266-748A-168581	Sequence 168581,	
c 8	60.5	35.8	1408	8	US-11-266-748A-183944	Sequence 183944,	
c 9	60.5	35.8	1493	8	US-11-266-748A-168580	Sequence 168580,	
c 10	60.5	35.8	1565	8	US-11-266-748A-19663	Sequence 19663, A	
c 11	60.5	35.8	1795	8	US-11-266-748A-249880	Sequence 249880,	
c 12	60.5	35.8	1795	8	US-11-266-748A-274644	Sequence 274644,	
13	60.5	35.8	1795	8	US-11-266-748A-310397	Sequence 310397,	
c 14	60.5	35.8	2046	8	US-11-266-748A-73892	Sequence 73892, A	
c 15	60.5	35.8	2046	8	US-11-266-748A-108070	Sequence 108070,	
16	60.5	35.8	2046	8	US-11-266-748A-126703	Sequence 126703,	
c 17	60	35.5	546	8	US-11-266-748A-207482	Sequence 207482,	
18	60	35.5	550	8	US-11-266-748A-361880	Sequence 361880,	
c 19	60	35.5	550	8	US-11-266-748A-445259	Sequence 445259,	
20	60	35.5	896	8	US-11-266-748A-117314	Sequence 117314,	
c 21	60	35.5	896	8	US-11-266-748A-159478	Sequence 159478,	
22	60	35.5	2135	8	US-11-266-748A-185503	Sequence 185503,	
23	60	35.5	2135	8	US-11-266-748A-192966	Sequence 192966,	
24	59.5	35.2	423	8	US-11-266-748A-115612	Sequence 115612,	
c 25	59.5	35.2	423	8	US-11-266-748A-157776	Sequence 157776,	
26	59.5	35.2	1901	9	US-11-218-305-20231	Sequence 20231, A	
27	59	34.9	1000	8	US-11-266-748A-393342	Sequence 393342,	
c 28	59	34.9	1000	8	US-11-266-748A-464388	Sequence 464388,	
c 29	59	34.9	1287	9	US-11-218-305-22060	Sequence 22060, A	
30	59	34.9	1414	8	US-11-266-748A-27774	Sequence 27774, A	
c 31	58	34.3	787	8	US-11-266-748A-68635	Sequence 68635, A	
c 32	58	34.3	787	8	US-11-266-748A-104963	Sequence 104963,	
33	58	34.3	787	8	US-11-266-748A-121446	Sequence 121446,	
34	58	34.3	1000	8	US-11-266-748A-221803	Sequence 221803,	
35	58	34.3	1000	8	US-11-266-748A-287165	Sequence 287165,	
c 36	58	34.3	1000	8	US-11-266-748A-338594	Sequence 338594,	
37	58	34.3	1000	8	US-11-266-748A-397780	Sequence 397780,	
c 38	58	34.3	1000	8	US-11-266-748A-468826	Sequence 468826,	
39	57	33.7	700	8	US-11-266-748A-480122	Sequence 480122,	
40	57	33.7	816	8	US-11-266-748A-354233	Sequence 354233,	
41	57	33.7	816	8	US-11-266-748A-384829	Sequence 384829,	

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:35:25 ; Search time 3516.55 Seconds
(without alignments)
787.138 Million cell updates/sec

Title: US-10-617-561-15
Perfect score: 169
Sequence: 1 XHWSHDWKPGFALALKALKKKALKKKLKKALKKKAL 33

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

```
-MODEL=frame+_p2n.model -DEV=xlp  
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102055_128/app_query.fasta_1  
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p  
-USER=US10617561@CGN_1_1_17145@runat_11082006_102055_128 -NCPU=6 -ICPU=3  
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120  
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : EST:*
1: gb_est1:*

2: gb_est3:*
 3: gb_est4:*
 4: gb_est5:*
 5: gb_est6:*
 6: gb_htc:*
 7: gb_est2:*
 8: gb_est7:*
 9: gb_est8:*
 10: gb_est9:*
 11: gb_gss1:*
 12: gb_gss2:*
 13: gb_gss3:*
 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length	DB	ID			
c	1	69	40.8	272	3	BQ391397			BQ391397 NISC_mq18
c	2	69	40.8	1039	14	DU940520			DU940520 367266 To
	3	69	40.8	1336	10	DV792849			DV792849 Hw-loin_3
	4	68.5	40.5	378	9	DN258017			DN258017 Meso07572
	5	68	40.2	424	2	BG897859			BG897859 HOA25-1-G
c	6	67.5	39.9	586	1	AV602344			AV602344 AV602344
	7	67	39.6	658	2	BF791971			BF791971 602252358
c	8	67	39.6	730	14	CT043835			CT043835 Sus scrofa
	9	66	39.1	509	3	BP958426			BP958426 BP958426
	10	66	39.1	526	3	BU613702			BU613702 UI-M-EW0-
	11	66	39.1	590	4	BX478955			BX478955 DKFZp686C
c	12	66	39.1	644	8	CV276430			CV276430 WS0179.B2
	13	66	39.1	790	9	CX623722			CX623722 H11_A1 Sp
	14	65.5	38.8	760	14	CT396333			CT396333 Sus scrofa
	15	65	38.5	374	7	BE235687			BE235687 143260 MA
	16	65	38.5	473	5	CF957818			CF957818 1694rsice
	17	64.5	38.2	227	1	AA877706			AA877706 nr09g06.s
c	18	64.5	38.2	510	1	AJ683647			AJ683647 AJ683647
c	19	64.5	38.2	510	2	BI680031			BI680031 457364 MA
c	20	64.5	38.2	592	4	BX915868			BX915868 BX915868
c	21	64.5	38.2	592	4	BX926799			BX926799 BX926799
c	22	64.5	38.2	636	3	BP165086			BP165086 BP165086
c	23	64.5	38.2	677	10	DV230344			DV230344 EST-AR167
c	24	64.5	38.2	687	8	CN004424			CN004424 ip46e03.g
c	25	64.5	38.2	697	10	DV224495			DV224495 EST-AR181
c	26	64.5	38.2	771	5	CJ018839			CJ018839 CJ018839
c	27	64.5	38.2	788	3	BP439064			BP439064 BP439064
c	28	64.5	38.2	833	4	BW971958			BW971958 BW971958
c	29	64.5	38.2	834	5	CJ029697			CJ029697 CJ029697
c	30	64.5	38.2	844	9	DN107178			DN107178 1104600 M
c	31	64.5	38.2	853	3	BP172960			BP172960 BP172960
c	32	64.5	38.2	859	4	BW979844			BW979844 BW979844
c	33	64.5	38.2	861	5	CJ023153			CJ023153 CJ023153
c	34	64.5	38.2	864	3	BP169610			BP169610 BP169610
c	35	64.5	38.2	868	4	BW976062			BW976062 BW976062
c	36	64	37.9	179	12	CC178380			CC178380 XD075 Bay
c	37	64	37.9	303	1	AV161371			AV161371 AV161371
	38	64	37.9	593	12	CE041369			CE041369 tigr-gss-

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:33:24 ; Search time 4111.77 Seconds
(without alignments)
886.481 Million cell updates/sec

Title: US-10-617-561-12
Perfect score: 184
Sequence: 1 FALALKALKKKLKKLKKALKKALS YAVALSQCALCRR 38

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102053_91/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss04
-USER=US10617561@CGN_1_1_6362@runat_11082006_102053_91 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_env:*

2: gb_pat:*
 3: gb_ph:*
 4: gb_pl:*
 5: gb_pr:*
 6: gb_ro:*
 7: gb_sts:*
 8: gb_sy:*
 9: gb_un:*
 10: gb_vi:*
 11: gb_ov:*
 12: gb_htg:*
 13: gb_in:*
 14: gb_om:*
 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				ID	Description
	No.	Score	Match	Length	DB	Query		
	1	87	47.3	539	2	AR079926	AR079926	Sequence
	2	87	47.3	539	2	AR178277	AR178277	Sequence
	3	87	47.3	539	2	AR478110	AR478110	Sequence
	4	84	45.7	468	5	HUMCGBBA3	K03183	Human chori
	5	84	45.7	475	5	HUMCGBEL03	K03189	Human chori
	6	84	45.7	498	5	BT006890	BT006890	Homo sapi
	7	84	45.7	498	8	AY889866	AY889866	Synthetic
	8	84	45.7	498	8	AY890611	AY890611	Synthetic
	9	84	45.7	498	8	AY892341	AY892341	Synthetic
	10	84	45.7	498	8	AY892342	AY892342	Synthetic
	11	84	45.7	498	8	AY893091	AY893091	Synthetic
	12	84	45.7	498	8	BT007573	BT007573	Synthetic
	13	84	45.7	516	5	BC069367	BC069367	Homo sapi
	14	84	45.7	519	5	BC106724	BC106724	Homo sapi
	15	84	45.7	520	5	BC106723	BC106723	Homo sapi
	16	84	45.7	524	5	BC069526	BC069526	Homo sapi
	17	84	45.7	530	2	BD078016	BD078016	Thyroid-s
	18	84	45.7	539	2	BD236914	BD236914	Chorionic
	19	84	45.7	539	2	AR345119	AR345119	Sequence
	20	84	45.7	539	2	AR360783	AR360783	Sequence
	21	84	45.7	539	2	AR399260	AR399260	Sequence
	22	84	45.7	539	2	AR481838	AR481838	Sequence
	23	84	45.7	539	2	AR590784	AR590784	Sequence
	24	84	45.7	539	5	HUMCGB	J00117	Human chori
c	25	84	45.7	549	2	AR154352	AR154352	Sequence
c	26	84	45.7	549	2	AR156976	AR156976	Sequence
c	27	84	45.7	549	2	BD140380	BD140380	Method fo
	28	84	45.7	555	2	CQ769367	CQ769367	Sequence
	29	84	45.7	575	2	AR154351	AR154351	Sequence
	30	84	45.7	575	2	AR156975	AR156975	Sequence
	31	84	45.7	575	2	BD140379	BD140379	Method fo
	32	84	45.7	587	2	AR257363	AR257363	Sequence
	33	84	45.7	607	5	BC103969	BC103969	Homo sapi
	34	84	45.7	607	5	BC103971	BC103971	Homo sapi
	35	84	45.7	611	5	BC103970	BC103970	Homo sapi
c	36	84	45.7	717	2	AR154332	AR154332	Sequence
c	37	84	45.7	717	2	AR154342	AR154342	Sequence

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:32:04 ; Search time 382.774 Seconds
(without alignments)
1038.259 Million cell updates/sec

Title: US-10-617-561-12
Perfect score: 184
Sequence: 1 FALALKALKKKLKKLKKALS YAVALSQCQCALCRR 38

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102051_79/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US10617561_@CGN_1_1_1975_@runat_11082006_102051_79 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_8:*
1: geneseqn1980s:*

2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002as:*
 7: geneseqn2002bs:*
 8: geneseqn2003as:*
 9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004as:*
 13: geneseqn2004bs:*
 14: geneseqn2005s:*
 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%					Description
	No.	Score	Match	Length	ID	
	1	87	47.3	539	2 AAV04780	Aav04780 Human cho
	2	87	47.3	539	2 AAV18517	Aav18517 Human bet
	3	87	47.3	539	2 AAV04779	Aav04779 Human cho
c	4	84	45.7	332	12 ACH88458	Ach88458 Human gen
	5	84	45.7	498	12 ADN49743	Adn49743 Beta subu
	6	84	45.7	498	13 ADU74419	Adu74419 Human cho
	7	84	45.7	498	14 AED73859	Aed73859 Human pla
	8	84	45.7	534	3 AAZ90609	Aaz90609 Human bet
	9	84	45.7	539	2 AAX25387	Aax25387 Human cho
	10	84	45.7	539	3 AAA73833	Aaa73833 Human cho
	11	84	45.7	539	11 ADM64531	Adm64531 Beta-huma
	12	84	45.7	539	12 ADH52593	Adh52593 Human cho
	13	84	45.7	539	12 ADH52556	Adh52556 Human cho
	14	84	45.7	539	12 ADK39744	Adk39744 DNA encod
	15	84	45.7	539	13 ADT90936	Adt90936 Human bet
	16	84	45.7	543	6 ADE50947	Ade50947 hCG-LH fu
c	17	84	45.7	549	4 AAD08808	Aad08808 Human sin
c	18	84	45.7	554	12 ACH74758	Ach74758 Human gen
	19	84	45.7	555	10 ADI62650	Adi62650 Human apo
	20	84	45.7	575	2 AAT03240	Aat03240 Human CG
	21	84	45.7	575	4 AAS08507	Aas08507 DNA encod
	22	84	45.7	575	4 AAD08807	Aad08807 Human sin
	23	84	45.7	579	2 AAQ14800	Aaq14800 Human cho
	24	84	45.7	587	2 AAZ31734	Aaz31734 Human cho
c	25	84	45.7	717	4 AAD08788	Aad08788 Human sin
c	26	84	45.7	717	4 AAD08800	Aad08800 Human sin
c	27	84	45.7	717	4 AAD08798	Aad08798 Human sin
	28	84	45.7	725	2 AAZ31742	Aaz31742 Human CG
	29	84	45.7	725	2 AAZ31751	Aaz31751 Human CG
	30	84	45.7	725	2 AAZ31750	Aaz31750 Human CG
c	31	84	45.7	726	4 AAD08796	Aad08796 Human sin
	32	84	45.7	732	13 ADQ83691	Adq83691 Human tum
	33	84	45.7	732	13 ADQ83690	Adq83690 Human tum
	34	84	45.7	743	2 AAT03233	Aat03233 Single ch
	35	84	45.7	743	2 AAT03231	Aat03231 Single ch
	36	84	45.7	743	2 AAT03219	Aat03219 Single ch
	37	84	45.7	743	4 AAS08499	Aas08499 DNA encod

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:51:34 ; Search time 120.102 Seconds
(without alignments)
888.020 Million cell updates/sec

Title: US-10-617-561-12
Perfect score: 184
Sequence: 1 FALALKALKKKLKKALKKALSVAVALSCQCALCRR 38

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102057_179/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss06p -USER=US10617561_@CGN_1_1_529_@runat_11082006_102057_179 -NCPU=6
-ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*

```

3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	87	47.3	539	2	US-08-709-924-1	Sequence 1, Appli
2	87	47.3	539	2	US-08-709-925-1	Sequence 1, Appli
3	87	47.3	539	3	US-08-709-948-1	Sequence 1, Appli
4	87	47.3	539	3	US-10-050-875-1	Sequence 1, Appli
5	84	45.7	539	3	US-09-220-415-1	Sequence 1, Appli
6	84	45.7	539	3	US-09-675-776-1	Sequence 1, Appli
7	84	45.7	539	3	US-09-676-739-1	Sequence 1, Appli
8	84	45.7	539	3	US-09-675-362-1	Sequence 1, Appli
9	84	45.7	539	3	US-09-677-152-1	Sequence 1, Appli
c 10	84	45.7	549	3	US-08-918-288-37	Sequence 37, Appl
c 11	84	45.7	549	3	US-09-282-357-37	Sequence 37, Appl
12	84	45.7	575	3	US-08-918-288-35	Sequence 35, Appl
13	84	45.7	575	3	US-09-282-357-35	Sequence 35, Appl
14	84	45.7	575	5	US-08-867-587B-35	Sequence 35, Appl
15	84	45.7	587	3	US-09-059-625-2	Sequence 2, Appli
c 16	84	45.7	717	3	US-08-918-288-7	Sequence 7, Appli
c 17	84	45.7	717	3	US-08-918-288-22	Sequence 22, Appl
c 18	84	45.7	717	3	US-08-918-288-25	Sequence 25, Appl
c 19	84	45.7	717	3	US-09-282-357-7	Sequence 7, Appli
c 20	84	45.7	717	3	US-09-282-357-22	Sequence 22, Appl
c 21	84	45.7	717	3	US-09-282-357-25	Sequence 25, Appl
22	84	45.7	725	3	US-09-059-625-36	Sequence 36, Appl
23	84	45.7	725	3	US-09-059-625-50	Sequence 50, Appl
24	84	45.7	725	3	US-09-059-625-55	Sequence 55, Appl
c 25	84	45.7	726	3	US-08-918-288-19	Sequence 19, Appl
c 26	84	45.7	726	3	US-09-282-357-19	Sequence 19, Appl
27	84	45.7	743	3	US-08-918-288-5	Sequence 5, Appli
28	84	45.7	743	3	US-08-918-288-20	Sequence 20, Appl
29	84	45.7	743	3	US-08-918-288-23	Sequence 23, Appl
30	84	45.7	743	3	US-09-282-357-5	Sequence 5, Appli
31	84	45.7	743	3	US-09-282-357-20	Sequence 20, Appl
32	84	45.7	743	3	US-09-282-357-23	Sequence 23, Appl
33	84	45.7	743	5	US-08-867-587B-5	Sequence 5, Appli
34	84	45.7	743	5	US-08-867-587B-20	Sequence 20, Appl
35	84	45.7	743	5	US-08-867-587B-23	Sequence 23, Appl
36	84	45.7	752	3	US-08-918-288-17	Sequence 17, Appl
37	84	45.7	752	3	US-09-282-357-17	Sequence 17, Appl
38	84	45.7	752	5	US-08-867-587B-17	Sequence 17, Appl
c 39	84	45.7	834	3	US-08-918-288-4	Sequence 4, Appli
c 40	84	45.7	834	3	US-09-282-357-4	Sequence 4, Appli
c 41	84	45.7	835	3	US-08-918-288-40	Sequence 40, Appl
c 42	84	45.7	835	3	US-09-282-357-40	Sequence 40, Appl
43	84	45.7	836	3	US-08-918-288-2	Sequence 2, Appli

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:58:24 ; Search time 1273.42 Seconds
(without alignments)
550.013 Million cell updates/sec

Title: US-10-617-561-12
Perfect score: 184
Sequence: 1 FALALKALKKKLKKALKKALS YAVALSCQCALCRR 38

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102100_235/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pt0 -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss06p
-USER=US10617561@CGN_1_1_5513@runat_11082006_102100_235 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*

```

2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
c	1	87	47.3	539	6	US-10-050-875-1	Sequence 1, Appli
	2	84	45.7	332	7	US-10-029-386-21653	Sequence 21653, A
	3	84	45.7	495	16	US-11-235-621-4	Sequence 4, Appli
	4	84	45.7	498	8	US-10-411-037-71	Sequence 71, Appl
	5	84	45.7	498	8	US-10-411-026-71	Sequence 71, Appl
	6	84	45.7	498	8	US-10-410-962-71	Sequence 71, Appl
	7	84	45.7	498	8	US-10-411-049-71	Sequence 71, Appl
	8	84	45.7	498	8	US-10-410-930-71	Sequence 71, Appl
	9	84	45.7	498	8	US-10-410-997-71	Sequence 71, Appl
	10	84	45.7	498	8	US-10-411-012-71	Sequence 71, Appl
	11	84	45.7	498	8	US-10-410-913-71	Sequence 71, Appl
	12	84	45.7	498	9	US-10-410-980-71	Sequence 71, Appl
	13	84	45.7	498	10	US-10-410-897-71	Sequence 71, Appl
	14	84	45.7	498	10	US-10-821-234-687	Sequence 687, App
	15	84	45.7	530	9	US-10-788-383-3	Sequence 3, Appli
c	16	84	45.7	539	3	US-09-466-320-15	Sequence 15, Appl
	17	84	45.7	554	7	US-10-029-386-7953	Sequence 7953, Ap
	18	84	45.7	879	16	US-11-219-339-3	Sequence 3, Appli
	19	84	45.7	880	8	US-10-734-564-57	Sequence 57, Appl
	20	84	45.7	893	3	US-09-760-294-3	Sequence 3, Appli
	21	84	45.7	893	3	US-09-760-294-5	Sequence 5, Appli
	22	84	45.7	893	3	US-09-760-294-6	Sequence 6, Appli
	23	84	45.7	893	3	US-09-760-294-7	Sequence 7, Appli
	24	84	45.7	893	3	US-09-760-294-8	Sequence 8, Appli
	25	84	45.7	893	3	US-09-760-294-9	Sequence 9, Appli
c	26	84	45.7	893	3	US-09-760-294-10	Sequence 10, Appl
	27	84	45.7	998	12	US-10-301-480-583005	Sequence 583005,
c	28	84	45.7	998	12	US-10-301-480-1196414	Sequence 1196414,
	29	84	45.7	1202	3	US-09-756-186-3	Sequence 3, Appli
	30	84	45.7	1202	9	US-10-724-226-3	Sequence 3, Appli
	31	84	45.7	1301	3	US-09-756-186-7	Sequence 7, Appli
	32	84	45.7	1301	9	US-10-724-226-7	Sequence 7, Appli
	33	84	45.7	1325	9	US-10-769-144-11	Sequence 11, Appl
	34	84	45.7	1325	10	US-10-903-191-11	Sequence 11, Appl
	35	84	45.7	1542	16	US-11-235-621-18	Sequence 18, Appl
	36	84	45.7	1842	9	US-10-769-144-9	Sequence 9, Appli

SCORE Search Results Details for Application 10617561 and Search Result us-10-617-561-12.p2n.rst.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:35:25 ; Search time 4049.36 Seconds
(without alignments)
787.138 Million cell updates/sec

Title: US-10-617-561-12
Perfect score: 184
Sequence: 1 FALALKALKKKLKKLKKALKKALS YAVALSCQCALCRR 38

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102055_128/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US10617561_@CGN_1_1_17145_@runat_11082006_102055_128 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*

2: gb_est3:*
 3: gb_est4:*
 4: gb_est5:*
 5: gb_est6:*
 6: gb_htc:*
 7: gb_est2:*
 8: gb_est7:*
 9: gb_est8:*
 10: gb_est9:*
 11: gb_gss1:*
 12: gb_gss2:*
 13: gb_gss3:*
 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query					ID	Description
	No.	Score	Match	Length	DB		
c	1	92	50.0	255	10	R63352	R63352 yi07h10.s1
	2	90	48.9	378	7	BF369834	BF369834 QV4-GN012
	3	88	47.8	905	3	BM810215	BM810215 AGENCOURT
c	4	87	47.3	248	10	H95381	H95381 yw60d07.s1
c	5	87	47.3	254	3	BU752621	BU752621 UI-1-BC0-
c	6	87	47.3	367	10	H94446	H94446 yw55f02.s1
c	7	87	47.3	473	1	AA400910	AA400910 zt71h09.s
c	8	87	47.3	473	10	N27302	N27302 yw71f12.s1
c	9	87	47.3	515	10	N30608	N30608 yw72c07.s1
c	10	87	47.3	526	1	AA644163	AA644163 af62d08.s
c	11	87	47.3	531	10	W71989	W71989 zd66b03.s1
c	12	87	47.3	548	10	N30036	N30036 yw80b11.s1
c	13	87	47.3	564	10	N32604	N32604 yw95d03.s1
c	14	87	47.3	593	10	N29730	N29730 yw78h03.s1
c	15	87	47.3	601	10	N32759	N32759 yw91b05.s1
	16	85	46.2	867	4	BX379814	BX379814 BX379814
	17	85	46.2	1108	3	BM909276	BM909276 AGENCOURT
	18	84	45.7	251	1	AA330413	AA330413 EST34462
c	19	84	45.7	255	5	CF527786	CF527786 UI-1-BC0-
c	20	84	45.7	258	5	CF527734	CF527734 UI-1-BC0-
c	21	84	45.7	260	3	BU752347	BU752347 UI-1-BC0-
c	22	84	45.7	266	10	H93668	H93668 yw55c12.s1
c	23	84	45.7	279	5	CF527738	CF527738 UI-1-BC0-
c	24	84	45.7	279	5	CF528202	CF528202 UI-1-BC0-
c	25	84	45.7	280	5	CF527893	CF527893 UI-1-BC0-
c	26	84	45.7	284	10	H93656	H93656 yw55a11.s1
c	27	84	45.7	291	3	BQ003972	BQ003972 UI-1-BC0-
c	28	84	45.7	299	5	CF527823	CF527823 UI-1-BC0-
c	29	84	45.7	299	5	CF528125	CF528125 UI-1-BC0-
c	30	84	45.7	305	3	BU752444	BU752444 UI-1-BC0-
c	31	84	45.7	308	5	CF528150	CF528150 UI-1-BC0-
c	32	84	45.7	309	3	BQ007333	BQ007333 UI-1-BC0-
c	33	84	45.7	309	5	CF528240	CF528240 UI-1-BC0-
c	34	84	45.7	313	3	BQ004094	BQ004094 UI-1-BC0-
c	35	84	45.7	313	3	BQ007393	BQ007393 UI-1-BC0-
c	36	84	45.7	313	3	BU752304	BU752304 UI-1-BC0-
c	37	84	45.7	313	3	BU752610	BU752610 UI-1-BC0-
c	38	84	45.7	313	5	CF527771	CF527771 UI-1-BC0-

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 12, 2006, 09:33:24 ; Search time 3570.74 Seconds
(without alignments)
886.481 Million cell updates/sec

Title: US-10-617-561-15
Perfect score: 169
Sequence: 1 XHWSHDWKPGFALALKALKKKALKKKLKKALKKAL 33

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10617561/runat_11082006_102053_91/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss04
-USER=US10617561@CGN_1_1_6362@runat_11082006_102053_91 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_env:*

2: gb_pat:*
 3: gb_ph:*
 4: gb_pl:*
 5: gb_pr:*
 6: gb_ro:*
 7: gb_sts:*
 8: gb_sy:*
 9: gb_un:*
 10: gb_vi:*
 11: gb_ov:*
 12: gb_htg:*
 13: gb_in:*
 14: gb_om:*
 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%		Query			DB	ID	Description
	No.	Score	Match	Length				
	1	82	48.5	710	11	AY307177	AY307177	Lampetra
	2	80	47.3	722	11	AY307176	AY307176	Lampetra
	3	80	47.3	723	11	AY307175	AY307175	Ichthyomy
	4	80	47.3	728	11	AY307174	AY307174	Ichthyomy
	5	80	47.3	732	11	AY307178	AY307178	Lampetra
	6	80	47.3	750	2	AR778646	AR778646	Sequence
	7	76	45.0	718	2	AR778647	AR778647	Sequence
	8	76	45.0	718	11	AY052628	AY052628	Petromyzo
	9	75	44.4	774	11	AY307172	AY307172	Geotria a
	10	75	44.4	790	2	AR778644	AR778644	Sequence
	11	72	42.6	666	11	AY307173	AY307173	Mordacia
c	12	70	41.4	183117	12	AC097012	AC097012	Sus scrof
	13	70	41.4	191474	5	AC018450	AC018450	Homo sapi
	14	69	40.8	676	2	AR778645	AR778645	Sequence
c	15	69	40.8	175569	6	AC102282	AC102282	Mus muscu
c	16	69	40.8	223318	12	AC095389	AC095389	Rattus no
c	17	69	40.8	269719	12	AC136277	AC136277	Rattus no
c	18	68	40.2	263287	12	AC171986	AC171986	Bos tauru
c	19	67	39.6	110000	15	AE010299_21	Continuation (22 o	
	20	66.5	39.3	110000	15	AE016877_47	Continuation (48 o	
c	21	66	39.1	29963	5	AL356859	AL356859	Human DNA
	22	66	39.1	167388	12	AC157445	AC157445	Sus scrof
c	23	66	39.1	168091	6	AC139553	AC139553	Mus muscu
	24	66	39.1	182733	6	AC123941	AC123941	Mus muscu
c	25	64.5	38.2	1618	14	SSC293581	AJ293581	Sus scrof
c	26	64.5	38.2	1730	2	I33464	I33464	Sequence 1
c	27	64.5	38.2	1730	2	I36536	I36536	Sequence 1
c	28	64.5	38.2	1730	2	I58393	I58393	Sequence 1
	29	64.5	38.2	185146	12	AC175181	AC175181	Bos tauru
	30	64	37.9	2468	5	BC053878	BC053878	Homo sapi
	31	64	37.9	60563	12	AC137682	AC137682	Homo sapi
	32	64	37.9	65002	12	AC136362	AC136362	Homo sapi
	33	64	37.9	110000	12	CR931980_2	Continuation (3 of	
c	34	64	37.9	158892	12	AC132819	AC132819	Homo sapi
c	35	64	37.9	163681	5	AL136992	AL136992	Human DNA
c	36	64	37.9	188340	5	AC135178	AC135178	Homo sapi
	37	64	37.9	204939	12	AC156047	AC156047	Bos tauru